

AMENDMENT

Please amend the subject application as follows:

IN THE CLAIMS:

1-30. (Cancelled)

Please add the following new claims:

31. (New) A method for categorizing a human patient suspected of having SMEI as having a high probability of having SMEI, the method comprising:
 - (1) analyzing a biological sample obtained from the human patient, the biological sample comprising the SCN1A gene of the human patient;
 - (2) detecting in the SCN1A gene of the human patient a G nucleotide at a position corresponding to position 517 of SEQ ID NO: 1; and
 - (3) categorizing the human patient as having a high probability of having SMEI.
32. (New) The method of claim 31, further comprising detecting a SCN1A gene mutation selected from the group consisting of: c301C→T; c512T→A; c596C→G; c677C→T; c715G→A; c2837G→A; c3714A→C; c4186T→G; c4321G→C; c4633A→G; c4934G→A; c5119T→G; c5347G→A; c41delT; c496insGTGAATC; c1687delC; c3231delA; c3561-3562delAA; c4062delT; c4526delA; c3022G→T; c4279C→T; IVS4+5G→A; and IVS3-13T→A.
33. (New) The method of claim 31, further comprising detecting a SCN1A gene mutation not associated with SMEI, wherein the mutation is selected from the group consisting of: c580G→A; c4439G→T; c4907G→A; c1724delT; and c5741-5742delAA.
34. (New) A method of detecting a mutated SCN1A gene, the method comprising detecting a mutation in a biological sample comprising the SCN1A gene, wherein the mutation is a G nucleotide at a position corresponding to position 517

of SEQ ID NO:1, wherein detection of the mutation is indicative of a mutated SCN1A gene in the sample.

35. (New) The method of claim 34, further comprising detecting a SCN1A gene mutation selected from the group consisting of: c301C→T; c512T→A; c596C→G; c677C→T; c715G→A; c2837G→A; c3714A→C; c4186T→G; c4321G→C; c4633A→G; c4934G→A; c5119T→G; c5347G→A; c41delT; c496insGTGAATC; c1687delC; c3231delA; c3561-3562delAA; c4062delT; c4526delA; c3022G→T; c4279C→T; IVS4+5G→A; and IVS3-13T→A.

36. (New) The method of claim 34, further comprising detecting a SCN1A gene mutation selected from the group consisting of: c580G→A; c4439G→T; c4907G→A; c1724delT; and c5741-5742delAA.